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"C"

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari

(ii) TITLE OF INVENTION: Bacterial Superantigen
Vaccines

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Charles H. Harris
(B) STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
(C) CITY: FORT DETRICK
(D) STATE: MARYLAND
(E) COUNTRY: USA
(F) ZIP: 21702-5012

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.5
(D) SOFTWARE: Microsoft Word 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/882,431
(B) FILING DATE: June 25, 1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Charles H. Harris
(B) REGISTRATION NUMBER: 34,616
(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: (301) 619-2065
(B) TELEFAX: (301) 619-7714

(2) INFORMATION FOR SEQUENCE ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAAAAAA CAGCATTAC ATTACTTTA TTCATTGCC	40
TAACGTTGAC AACAAAGTCCA CTTGTAAATG GTAGCGAGAA	80
AAGCGAAGAA ATAAATGAAA AAGATTGCG AAAAAAGTCT	120
GAATTGCAGG GAACAGCTT AGGCAATCTT AAACAAATCT	160
ATTATTACAA TGAAAAGCT AAAACTGAAA ATAAAGAGAG	200
TCACGATCAA TTTCGACAGC ATACTATATT GTTTAAAGGC	240
TTTTTACAG ATCATTCTG GTATAACGAT TTATTAGTAC	280
GTTTGATTC AAAGGATATT GTTGATAAAT ATAAAGGGAA	320
AAAAGTAGAC TTGTATGGTG CTTATGCTGG TTATCAATGT	360
CGGGGTGGTA CACCAAACAA AACAGCTTGT ATGTATGGTG	400
GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA	440
AAAAGTGCCG ATCAATTAT GGCTAGACGG TAAACAAAAT	480
ACAGTACCTT TGGAAACGGT TAAAACGAAT AAGAAAAATG	520
TAACTGTTCA GGAGTTGGAT CTTCAAGCAA GACGTTATT	560
ACAGGAAAAA TATAATTAT ATAACCTCTGA TGTTTTGAT	600
GGGAAGGTTTC AGAGGGGATT AATCGTGTTC CATACTTCTA	640
CAGAACCTTC GGTAAATTAC GATTTATTG GTGCTCAAGG	680
ACAGTATTCA AATACACTAT TAAGAATATA TAGAGATAAT	720
AAAACGATTA ACTCTGAAAA CATGCATATT GATATATATT	760
TATATACAAG TTAAACATGG TAGTTTGAC CAACGTAATG	800
TTCAGATTAT TATGAACCGA GAATAATCTA	830

(3) INFORMATION FOR SEQUENCE ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257

- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Lys	Thr	Ala	Phe	Thr	Leu	Leu	Leu	1	5	10
Phe	Ile	Ala	Leu	Thr	Leu	Thr	Thr	Ser	Pro	15	20	
Leu	Val	Asn	Gly	Ser	Glu	Lys	Ser	Glu	Glu	25	30	
Ile	Asn	Glu	Lys	Asp	Leu	Arg	Lys	Lys	Ser	35	40	
Glu	Leu	Gln	Gly	Thr	Ala	Leu	Gly	Asn	Leu	45	50	
Lys	Gln	Ile	Tyr	Tyr	Tyr	Asn	Glu	Lys	Ala	55	60	
Lys	Thr	Glu	Asn	Lys	Glu	Ser	His	Asp	Gln	65	70	
Phe	Arg	Gln	His	Thr	Ile	Leu	Phe	Lys	Gly	75	80	
Phe	Phe	Thr	Asp	His	Ser	Trp	Tyr	Asn	Asp	85	90	
Leu	Leu	Val	Arg	Phe	Asp	Ser	Lys	Asp	Ile	95	100	
Val	Asp	Lys	Tyr	Lys	Gly	Lys	Lys	Val	Asp	105	110	
Leu	Tyr	Gly	Ala	Tyr	Ala	Gly	Tyr	Gln	Cys	115	120	
Ala	Gly	Gly	Thr	Pro	Asn	Lys	Thr	Ala	Cys	125	130	
Met	Tyr	Gly	Gly	Val	Thr	Leu	His	Asp	Asn	135	140	
Asn	Arg	Leu	Thr	Glu	Glu	Lys	Lys	Val	Pro	145	150	
Ile	Asn	Leu	Trp	Leu	Asp	Gly	Lys	Gln	Asn	155	160	

Thr Val Pro Leu Glu Thr Val Lys Thr Asn
 165 170
 Lys Lys Asn Val Thr Val Gln Glu Leu Asp
 175 180
 Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys
 185 190
 Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
 195 200
 Gly Lys Val Gln Arg Gly Leu Ile Val Phe
 205 210
 His Thr Ser Thr Glu Pro Ser Val Asn Tyr
 215 220
 Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser
 225 230
 Asn Thr Leu Ile Arg Ile Tyr Arg Asp Asn
 235 240
 Lys Thr Ile Asn Ser Glu Asn Met His Ile
 245 250
 Asp Ile Tyr Leu Tyr Thr Ser
 255

(4) INFORMATION FOR SEQUENCE ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAGAAAAG CGAAGAAATA AATGAAAAG ATTTGCGAAA	40
AAAGTCTGAA TTGCAGGGAA CAGCTTTAGG CAATCTTAAA	80
CAAATCTATT ATTACAATGA AAAAGCTAAA ACTGAAAATA	120
AAGAGAGTCA CGATCAATT CGACAGCATA CTATATTGTT	160
TAAAGGCTTT TTTACAGATC ATT CGTGGTA TAACGATTAA	200

TTAGTACGTT	TTGATTCAAA	GGATATTGTT	GATAAATATA	240
AAGGGAAAAA	AGTAGACTTG	TATGGTGCTT	ATGCTGGTTA	280
TCAATGTGCG	GGTGGTACAC	CAAACAAAAC	AGCTTGTATG	320
TATGGTGGTG	TAACGTTACA	TGATAATAAT	CGATTGACCG	360
AAGAGAAAAA	AGTGCCGATC	AATTTATGGC	TAGACGGTAA	400
ACAAAATACA	GTACCTTGG	AAACGGTTAA	AACGAATAAG	440
AAAAATGTAA	CTGTTCAGGA	GTTGGATCTT	CAAGCAAGAC	480
GTTATTTACA	GGAAAAATAT	AATTTATATA	ACTCTGATGT	520
TTTGATGGG	AAGGTTCAGA	GGGGATTAAT	CGTGTTCAT	560
ACTTCTACAG	AACCTTCGGT	TAATTACGAT	TTATTTGGTG	600
CTCAAGGACA	GTATTCAAAT	ACACTATTAA	GAATATATAG	640
AGATAATAAA	ACGATTAAC	CTGAAAACAT	GCATATTGAT	680
ATATATTTAT	ATACAAGTTA	AACATGGTAG	TTTGACCAA	720
CGTAATGTTC	AGATTATTAT	GAACCGAGAA	TAATCTA	757

(5) INFORMATION FOR SEQUENCE ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
5 10

Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly
15 20

Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr
25 30

Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
35 40

Lys Glu Ser His Asp Gln Phe Arg Gln His
45 50

Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp
55 60

His Ser Trp Tyr Asn Asp Leu Leu Val Arg
65 70

Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr
75 80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala
85 90

Tyr Ala Gly Tyr Gln Cys Ala Gly Gly Thr
95 100

Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly
105 110

Val Thr Leu His Asp Asn Asn Arg Leu Thr
115 120

Glu Glu Lys Lys Val Pro Ile Asn Leu Trp
125 130

Leu Asp Gly Lys Gln Asn Thr Val Pro Leu
135 140

Glu Thr Val Lys Thr Asn Lys Lys Asn Val
145 150

Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
155 160

Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr
165 170

Asn Ser Asp Val Phe Asp Gly Lys Val Gln
175 180

Arg Gly Leu Ile Val Phe His Thr Ser Thr
185 190

Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
195 200

Ala Gln Gly Gln Tyr Ser Asn Thr Leu Leu
205 210

Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn
215 220

Ser Glu Asn Met His Ile Asp Ile Tyr Leu
 225 230
 Tyr Thr Ser

(6) INFORMATION FOR SEQUENCE ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG	40
TTAAAGATGT TTTCGTATAT AAGTTTAGGT GATGTATAGT	80
TACTTAATTT TAAAAGCATA ACTTAATTAA TATAAATAAC	120
ATGAGATTAT TAAATATAAT TAAGTTCTT TTAATGTTTT	160
TTTAATTGAA TATTTAAGAT TATAACATAT ATTTAAAGTG	200
TATCTAGATA CTTTTGGGA ATGTTGGATA AAGGAGATAA	240
AAAATGTATA AGAGATTATT TATTCACAT GTAATTTGA	280
TATTCGCACT GATATTAGTT ATTTCTACAC CCAACGTTT	320
AGCAGAGAGT CAACCAGATC CTAAACCAGA TGAGTTGCAC	360
AAATCGAGTA AATTCACTGG TTTGATGGAA GATATGAAAG	400
TTTTGTATGA TGATAATCAT GTATCAGCAA TAAACGTTAA	440
ATCTATAGAT CAATTCTAT ACTTGACTT AATATATTCT	480
ATTAAGGACA CTAAGTTAGG GGATTATGAT AATGTTCGAG	520
TCGAATTTAA AAACAAAGAT TTAGCTGATA AATACAAAGA	560
TAAATACGTA GATGTGTTG GAGCTAATTA TTATTATCAA	600
TGTTATTTTT CTAAAAAAAC GAATGATATT AATTCGCATC	640
AAACTGACAA ACGAAAAACT TGTATGTATG GTGGTGTAAC	680

TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT	720
ACTGTTCGGG TATTTGAAGA TGGTAAAAT TTATTATCTT	760
TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
ATTAGATTAC CTAACTCGTC ACTATTTGGT GAAAAATAAA	840
AAACTCTATG AATTTAACAA CTCGCCTTAT GAAACGGGAT	880
ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
CATGATGCCT GCACCAGGAG ATAAATTGC CCAATCTAAA	960
TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
AATTAAGGCA GGCAC TTATA GAGTACCTGC CTTTTCTAAT	1120
ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
TAGCATTAAAC CCCTTGTGTC CATTATAGTT TTCACCAACT	1200
TTAGCTGAAA TTGGGGGATC ATTTTTATCT TTACTATGGA	1240
TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTTCTCTT	1280
TAATTTGTCA GTTAATTTT TCCATGCATC ATTTGCGTCA	1320
AACCTATTTC CATTGGATT TATTCTTGAC AAATCAATTC	1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAAAATT	1400
ACTAAAGTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT	1480
CATTTGCTGT TTTATCGATA ATATTTGCTT CTTTCAAAGC	1520
ATCTCTTACA TTTTCCATA AGTCTCTATC TGTTATTTCA	1560
GAAGCCTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AAACTAAAGC	1640
ACTTGCTATC AATGTTCTTGT TTAATAGTTT TTTATTCTT	1680
TTATTTCTC CTATAACTTA TTTGCAATCG AT	1712

(7) INFORMATION FOR SEQUENCE ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Tyr	Lys	Arg	Leu	Phe	Ile	Ser	His	Val		
				5						10	
Ile	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Val	Ile		
				15						20	
Ser	Thr	Pro	Asn	Val	Leu	Ala	Glu	Ser	Gln		
				25						30	
Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys		
				35						40	
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asp		
				45						50	
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val		
				55						60	
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln		
				65						70	
Phe	Leu	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile		
				75						80	
Lys	Asp	Thr	Lys	Leu	Gly	Asp	Tyr	Asp	Asn		
				85						90	
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu		
				95						100	
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp		
				105						110	
Val	Phe	Gly	Ala	Asn	Tyr	Tyr	Tyr	Gln	Cys		
				115						120	
Tyr	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn		
				125						130	
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys		
				135						140	

Met Tyr Gly Gly Val Thr Glu His Asn Gly
 145 150
 Asn Gln Leu Asp Lys Tyr Arg Ser Ile Thr
 155 160
 Val Arg Val Phe Glu Asp Gly Lys Asn Leu
 165 170
 Leu Ser Phe Asp Val Gln Thr Asn Lys Lys
 175 180
 Lys Val Thr Ala Gln Glu Leu Asp Tyr Leu
 185 190
 Thr Arg His Tyr Leu Val Lys Asn Lys Lys
 195 200
 Leu Tyr Glu Phe Asn Asn Ser Pro Tyr Glu
 205 210
 Thr Gly Tyr Ile Lys Phe Ile Glu Asn Glu
 215 220
 Asn Ser Phe Trp Tyr Asp Met Met Pro Ala
 225 230
 Pro Gly Asp Lys Phe Ala Gln Ser Lys Tyr
 235 240
 Leu Met Met Tyr Asn Asp Asn Lys Met Val
 245 250
 Asp Ser Lys Asp Val Lys Ile Glu Val Tyr
 255 260
 Leu Thr Thr Lys Lys Lys
 265

(8) INFORMATION FOR SEQUENCE ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAACTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG 40

TTAAAGATGT TTTCGTATAT AAGTTAGGT GATGTATAGT	80
TACTTAATT TAAAAGCATA ACTTAATTAA TATAAATAAC	120
ATGAGATTAT TAAATATAAT TAAGTTCTT TTAATGTTT	160
TTTAATTGAA TATTTAAGAT TATAACATAT ATTTAAAGTG	200
TATCTAGATA CTTTTGGGA ATGTTGGATA AAGGAGATAA	240
AAAATGTATA AGAGATTATT TATTCACAT GTAATTTGA	280
TATTCGCACT GATATTAGTT ATTTCTACAC CCAACGTTT	320
AGCAGAGAGT CAACCAGATC CTAAACCAGA TGAGTTGCAC	360
AAATCGAGTA AATTCACTGG TTTGATGGAA AATATGAAAG	400
TTTTGTATGA TGATAATCAT GTATCAGCAA TAAACGTTAA	440
ATCTATAGAT CAATTCGAT ACTTTGACTT AATATATTCT	480
ATTAAGGACA CTAAGTTAGG GAATTATGAT AATGTTCGAG	520
TCGAATTAA AAACAAAGAT TTAGCTGATA AATACAAAGA	560
TAAATACGTA GATGTGTTG GAGCTAATGC TTATTATCAA	600
TGTGCTTTT CTAAAAAAAC GAATGATATT AATTCGCATH	640
AAACTGACAA ACGAAAAACT TGTATGTATG GTGGTGTAAC	680
TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT	720
ACTGTTCGGG TATTTGAAGA TGGTAAAAT TTATTATCTT	760
TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
ATTAGATTAC CTAACTCGTC ACTATTGGT GAAAAATAAA	840
AAACTCTATG AATTTAACAA CTCGCCTTAT GAAACGGGAT	880
ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
CATGATGCCT GCACCAGGAG ATAAATTGAA CCAATCTAAA	960
TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
AATTAAGGCA GGCACTTATA GAGTACCTGC CTTTCTAAT	1120

ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
TAGCATTAAAC CCCTTGTGTC CATTATAGTT TTCACCAACT	1200
TTAGCTGAAA TTGGGGGATC ATTTTATCT TTACTATGGA	1240
TAGTTACTGT GTCGCCGTTT TTAACGATTG GTTTCTCTTT	1280
TAATTTGTCA GTTAATTTT TCCATGCATC ATTTGCGTCA	1320
AACCTATTTC CATTGGATT TATTCTTGAC AAATCAATT	1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAAAATT	1400
ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
TCGCCACCAT TATTAAATT GTACGTAACA CCAACTGTCT	1480
CATTTGCTGT TTTATCGATA ATATTTGCTT CTTTCAAAGC	1520
ATCTCTTACA TTTTCCATA AGTCTCTATC TGTTATTCA	1560
GAAGCCTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AAACTAAAGC	1640
ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCA	1680
TTATTTCTC CTATAACTTA TTTGCAATCG AT	1712

(9) INFORMATION FOR SEQUENCE ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Tyr	Lys	Arg	Leu	Phe	Ile	Ser	His	Val
				5				10	

Ile	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Val	Ile
				15				20	

Ser	Thr	Pro	Asn	Val	Leu	Ala	Glu	Ser	Gln
				25				30	

Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys
				35					40
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asn
				45					50
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val
				55					60
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln
				65					70
Phe	Arg	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile
				75					80
Lys	Asp	Thr	Lys	Leu	Gly	Asn	Tyr	Asp	Asn
				85					90
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu
				95					100
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp
				105					110
Val	Phe	Gly	Ala	Asn	Ala	Tyr	Tyr	Gln	Cys
				115					120
Ala	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn
				125					130
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys
				135					140
Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly
				145					150
Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr
				155					160
Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu
				165					170
Leu	Ser	Phe	Asp	Val	Gln	Tyr	Asn	Lys	Lys
				175					180
Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu
				185					190
Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys
				195					200
Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu
				205					210

Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Glu
				215				220	
Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala
				225				230	
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr
				235				240	
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val
				245				250	
Asp	Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr
				255				260	
Leu	Thr	Thr	Lys	Lys	Lys				
				265					

(10) INFORMATION FOR SEQUENCE ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGTCAAC	CAGATCCTAA	ACCAGATGAG	TTGCACAAAT	40
CGAGTAAATT	CACTGGTTG	ATGGAAAATA	TGAAAGTTTT	80
GTATGATGAT	AATCATGTAT	CAGCAATAAA	CGTTAAATCT	120
ATAGATCAAT	TTCGATACTT	TGACTTAATA	TATTCTATTA	160
AGGACACTAA	GTTAGGGAAT	TATGATAATG	TTCGAGTCGA	200
ATTTAAAAAC	AAAGATTTAG	CTGATAAATA	CAAAGATAAA	240
TACGTAGATG	TGTTTGGAGC	TAATGCTTAT	TATCAATGTG	280
CTTTTTCTAA	AAAAACGAAT	GATATTAATT	CGCATCAAAC	320
TGACAAACGA	AAAACTTGTA	TGTATGGTGG	TGTAACTGAG	360
CATAATGGAA	ACCAATTAGA	TAAATATAGA	AGTATTACTG	400
TTCGGGTATT	TGAAGATGGT	AAAAATTAT	TATCTTTGA	440

CGTACAAACT AATAAGAAAA AGGTGACTGC TCAAGAATTA	480
GATTACCTAA CTCGTCACTA TTTGGTGAAA AATAAAAAAC	520
TCTATGAATT TAACAACTCG CCTTATGAAA CGGGATATAT	560
TAAATTTATA GAAAATGAGA ATAGCTTTG GTATGACATG	600
ATGCCTGCAC CAGGAGATAA ATTGACCAA TCTAAATATT	640
TAATGATGTA CAATGACAAT AAAATGGTTG ATTCTAAAGA	680
TGTGAAGATT GAAGTTTATC TTACGACAAA GAAAAAGTGA	720
AATTATATTT TAGAAAAGTA AATATGAAGA GTTAGTAATT	760
AAGGCAGGCA CTTATAGAGT ACCTGCCTT TCTAATATTA	800
TTTAGTTATA GTTATTTTG TTATATCTCT CTGATTTAGC	840
ATTAACCCCT TGTTGCCATT ATAGTTTCAC CAACTTTAG	880
CTGAAATTGG GGGATCATT TTATCTTAC TATGGATAGT	920
TAATGTGTCG CCGTTTTAA CGATTGTTT CTCTTTAAT	960
TTGTCAGTTA ATTTTTCCA TGCATCATT GCGTCAAACC	1000
TATTTCCATT TGGATTATT CTTGACAAAT CAATTCTTT	1040
AACACTATCG GTATTAATCG GCTTGTATT AAAATTACTA	1080
AGTCATCTA AATCAGCTGT ACCCGTAATA CTACTTCGC	1120
CACCATTATT TAAATTGTAC GTAACACCAA CTGTCTCATT	1160
TGCTGTTTA TCGATAATAT TTGCTTCTT CAAAGCATCT	1200
CTTACATTTC TCCATAAGTC TCTATCTGTT ATTCAGAAG	1240
CCTTGCAAC GTTATTAATA CCATTATAAT TTGAAGAAGA	1280
ATGAAAACCT GAACCTACTG TTGTTAAAAC TAAAGCACTT	1320
GCTATCAATG TTCTGTTAA TAGTTTTTA TTCATTTAT	1360
TTTCTCCTAT AACTTATTG CAATCGAT	1388

(11) INFORMATION FOR SEQUENCE ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239

- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Gln Pro Asp Pro Lys Pro Asp Glu
5 10

Leu His Lys Ser Ser Lys Phe Thr Gly Leu
15 20

Met Glu Asn Met Lys Val Leu Tyr Asp Asp
25 30

Asn His Val Ser Ala Ile Asn Val Lys Ser
35 40

Ile Asp Gln Phe Arg Tyr Phe Asp Leu Ile
45 50

Tyr Ser Ile Lys Asp Thr Lys Leu Gly Asn
55 60

Tyr Asp Asn Val Arg Val Glu Phe Lys Asn
65 70

Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys
75 80

Tyr Val Asp Val Phe Gly Ala Asn Ala Tyr
85 90

Tyr Gln Cys Ala Phe Ser Lys Lys Thr Asn
95 100

Asp Ile Asn Ser His Gln Thr Asp Lys Arg
105 110

Lys Thr Cys Met Tyr Gly Gly Val Thr Glu
115 120

His Asn Gly Asn Gln Leu Asp Lys Tyr Arg
125 130

Ser Ile Thr Val Arg Val Phe Glu Asp Gly
135 140

Lys Asn Leu Leu Ser Phe Asp Val Gln Thr
145 150

Asn Lys Lys Lys Val Thr Ala Gln Glu Leu

	155	160
Asp Tyr Leu Thr Arg His Tyr Leu Val Lys		
165	170	
Asn Lys Lys Leu Tyr Glu Phe Asn Asn Ser		
175	180	
Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile		
185	190	
Glu Asn Glu Asn Ser Phe Trp Tyr Asp Met		
195	200	
Met Pro Ala Pro Gly Asp Lys Phe Asp Gln		
205	210	
Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn		
215	220	
Lys Met Val Asp Ser Lys Asp Val Lys Ile		
225	230	
Glu Val Tyr Leu Thr Thr Lys Lys Lys		
235		

(12) INFORMATION FOR SEQUENCE ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAAGGAGAAT TAAAAATGAA TAAAAAATTA CTAATGAATT	40
TTTTTATCGT AAGCCCTTG TTGCTTGCGA CAACTGCTAC	80
AGATTTTACCC CCTGTTCCCT TATCATCTAA TCAAATAATC	120
AAAAGTCGAA AAGCATCTAC AAACGATAAT ATAAAGGATT	160
TGCTAGACTG GTATAGTAGT GGGTCTGACA CTTTTACAAA	200
TAGTGAAGTT TTAGATAATT CCAGAGGATC TATGCGTATA	240
AAAAACACAG ATGGCAGCAT CAGCTTGATA ATTTTTCCGA	280

GTCCTTATTA TAGCCCTGCT TTTACAAAAG GGGAAAAAGT	320
TGACTTAAAC ACAAAAAGAA CTAAAAAAAG CCAACATACT	360
AGCGAAGGAA CTTATATCCA TTTCCAAATA AGTGGCGTTA	400
CAAATACTGA AAAATTACCT ACTCCAATAG AACTACCTTT	440
AAAAGTTAAG GTTCATGGTA AAGATAGCCC CTTAAAGTAT	480
GGGCCAAAGT TCGATAAAAA ACAATTAGCT ATATCAACTT	520
TAGACTTTGA AATTCTGTAT CAGCTAACTC AAATACATGG	560
ATTATATCGT TCAAGCGATA AAACGGGTGG TTATTGGAAA	600
ATAACAATGA ATGACGGATC CACATATCAA AGTGATTAT	640
CTAAAAAGTT TGAATACAAT ACTGAAAAAC CACCTATAAA	680
TATTGATGAA ATAAAAACTA TAGAAGCAGA AATTAATTAA	720
TTTACCACTT T	731

(13) INFORMATION FOR SEQUENCE ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asn	Lys	Lys	Leu	Leu	Met	Asn	Phe	Phe	
				5				10		
Ile	Val	Ser	Pro	Leu	Leu	Leu	Ala	Thr	Thr	
				15				20		
Ala	Thr	Asp	Phe	Thr	Pro	Val	Pro	Leu	Ser	
				25				30		
Ser	Asn	Gln	Ile	Ile	Lys	Thr	Ala	Lys	Ala	
				35				40		
Ser	Thr	Asn	Asp	Asn	Ile	Lys	Asp	Leu	Leu	
				45				50		
Asp	Trp	Tyr	Ser	Ser	Gly	Ser	Asp	Thr	Phe	
				55				60		

Thr Asn Ser Glu Val Leu Asp Asn Ser Arg
65 70

Gly Ser Met Arg Ile Lys Asn Thr Asp Gly
75 80

Ser Ile Ser Leu Ile Ile Phe Pro Ser Pro
85 90

Tyr Tyr Ser Pro Ala Phe Thr Lys Gly Glu
95 100

Lys Val Asp Leu Asn Thr Lys Arg Thr Lys
105 110

Lys Ser Gln His Thr Ser Glu Gly Thr Tyr
115 120

Ile His Phe Gln Ile Ser Gly Val Thr Asn
125 130

Thr Glu Lys Leu Pro Thr Pro Ile Glu Leu
135 140

Pro Leu Lys Val Lys Val His Gly Lys Asp
145 150

Ser Pro Leu Lys Tyr Gly Pro Lys Phe Asp
155 160

Lys Lys Gln Leu Ala Ile Ser Thr Leu Asp
165 170

Phe Glu Ile Arg His Gln Leu Thr Gln Ile
175 180

His Gly Leu Tyr Arg Ser Ser Asp Lys Thr
185 190

Gly Gly Tyr Trp Lys Ile Thr Met Asn Asp
195 200

Gly Ser Thr Tyr Gln Ser Asp Leu Ser Lys
205 210

Lys Phe Glu Tyr Asn Thr Glu Lys Pro Pro
215 220

Ile Asn Ile Asp Glu Ile Lys Thr Ile Glu
225 230

Ala Glu Ile Asn

(14) INFORMATION FOR SEQUENCE ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCATTAAAT ATAATTAATT TTCTTTAAT ATTTTTTAA	40
TTGAATATTT AAGATTATAA GATATATTAA AAGTGTATCT	80
AGATACTTT TGGAATGTT GGATGAAGGA GATAAAAATG	120
AATAAGAGTC GATTTATTTC ATGCGTAATT TTGATATTG	160
CACTTATACT AGTTCTTTT ACACCCAACG TATTAGCAGA	200
GAGCCAACCA GACCCTACGC CAGATGAGTT GCACAAAGCG	240
AGTAAATTCA CTGGTTGAT GGAAAATATG AAAGTTTAT	280
ATGATGATCA TTATGTATCA GCAACTAAAG TTAAGTCTGT	320
AGATAAAATTT AGGGCACATG ATTTAATTAA TAACATTAGT	360
GATAAAAAC TGAAAATTA TGACAAAGTG AAAACAGAGT	400
TATTAATGA AGGTTAGCA AAGAAGTACA AAGATGAAGT	440
AGTTGATGTG TATGGATCAA ATTACTATGT AAACTGCTAT	480
TTTCATCCA AAGATAATGT AGGTAAAGTT ACAGGTGGCA	520
AAACTTGTAT GTATGGAGGA ATAACAAAAC ATGAAGGAAA	560
CCACTTTGAT AATGGGAACT TACAAAATGT ACTTATAAGA	600
GTTTATGAAA ATAAAAGAAA CACAATTCT TTTGAAGTGC	640
AAACTGATAA GAAAAGTGT A CAGCTCAAG AACTAGACAT	680
AAAAGCTAGG AATTTTTAA TTAATAAAA AAATTTGTAT	720
GAGTTAACCA GTTCACCATA TGAAACAGGA TATATAAAAT	760
TTATTGAAAA TAACGGCAAT ACTTTTGGT ATGATATGAT	800

GCCTGCACCA GGCGATAAGT TTGACCAATC TAAATATT	840
ATGATGTACA ACGACAATAA AACGGTTGAT TCTAAAAGTG	880
TGAAGATAGA AGTCCACCTT ACAACAAAGA ATGGATAATG	920
TTAATCCGAT TTTGATATAA AAAGTGAAAG TATTAGATAT	960
ATTTGAAAGG TAAGTACTTC GGTGCTTGCC TTTTTAGGAT	1000
GCATATATAT AGATTAAACC GCACTTCTAT ATTAATAGAA	1040
AGTGCGGTTA TTTATACACT CAATCTAAC TATAATAATT	1080
GGAATCATCT TCAAA	1095

(15) INFORMATION FOR SEQUENCE ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asn Lys Ser Arg Phe Ile Ser Cys Val	
5	10
Ile Leu Ile Phe Ala Leu Ile Leu Val Leu	
15	20
Phe Thr Pro Asn Val Leu Ala Glu Ser Gln	
25	30
Pro Asp Pro Thr Pro Asp Glu Leu His Lys	
35	40
Ala Ser Lys Phe Thr Gly Leu Met Glu Asn	
45	50
Met Lys Val Leu Tyr Asp Asp His Tyr Val	
55	60
Ser Ala Thr Lys Val Lys Ser Val Asp Lys	
65	70
Phe Arg Ala His Asp Leu Ile Tyr Asn Ile	
75	80

Ser Asp Lys Lys Leu Lys Asn Tyr Asp Lys
 85 90
 Val Lys Thr Glu Leu Leu Asn Glu Gly Leu
 95 100
 Ala Lys Lys Tyr Lys Asp Glu Val Val Asp
 105 110
 Val Tyr Gly Ser Asn Tyr Tyr Val Asn Cys
 115 120
 Tyr Phe Ser Ser Lys Asp Asn Val Gly Lys
 125 130
 Val Thr Gly Gly Lys Thr Cys Met Tyr Gly
 135 140
 Gly Ile Thr Lys His Glu Gly Asn His Phe
 145 150
 Asp Asn Gly Asn Leu Gln Asn Val Leu Ile
 155 160
 Arg Val Tyr Glu Asn Lys Arg Asn Thr Ile
 165 170
 Ser Phe Glu Val Gln Thr Asp Lys Lys Ser
 175 180
 Val Thr Ala Gln Glu Leu Asp Ile Lys Ala
 185 190
 Arg Asn Phe Leu Ile Asn Lys Lys Asn Leu
 195 200
 Tyr Glu Phe Asn Ser Ser Phe Tyr Glu Thr
 205 210
 Gly Tyr Ile Lys Phe Ile Glu Asn Asn Gly
 215 220
 Asn Thr Phe Trp Tyr Asp Met Met Pro Ala
 225 230
 Pro Gly Asp Lys Phe Asp Gln Ser Lys Tyr
 235 240
 Leu Met Met Tyr Asn Asp Asn Lys Thr Val
 245 250
 Asp Ser Lys Ser Val Lys Ile Glu Val His
 255 260

Leu Thr Thr Lys Asn Gly
265

(16) INFORMATION FOR SEQUENCE ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCATGTTGA CAGCTTATCA TCGATAAGCT TACTTTTCGA	40
ATCAGGTCTA TCCTTGAAAC AGGTGCAACA TAGATTAGGG	80
CATGGAGATT TACCAAGACAA CTATGAACGT ATATACTCAC	120
ATCACGCAAT CGGCAATTGA TGACATTGGA ACTAAATTCA	160
ATCAATTGT TACTAACAAAG CAACTAGATT GACAACTAAT	200
TCTCAACAAA CGTTAATTAA ACAACATTCA AGTAACCTCCC	240
ACCAAGCTCCA TCAATGCTTA CCGTAAGTAA TCATAACTTA	280
CTAAAACCTT GTTACATCAA GGTTTTTCT TTTTGTCTTG	320
TTCATGAGTT ACCATAACTT TCTATATTAT TGACAACTAA	360
ATTGACAACCTT CTTCAATTAT TTTTCTGTCT ACTCAAAGTT	400
TTCTTCATTT GATATAGTCT AATTCCACCA TCACCTCTTC	440
CACTCTCTCT ACCGTCACAA CTTCATCATC TCTCACTTT	480
TCGTGTGGTA ACACATAATC AAATATCTTT CCGTTTTAC	520
GCACATATCGC TACTGTGTCA CCTAAAATAT ACCCCTTATC	560
AATCGCTTCT TTAAACTCAT CTATATATAA CATATTCAT	600
CCTCCTACCT ATCTATTCTGT AAAAAGATAA AAATAACTAT	640
TGTTTTTTTT GTTATTTTAT AATAAAATTA TTAATATAAG	680
TTAATGTTTT TTAAAAATAT ACAATTAT TCTATTTATA	720

GTAGCTATT TTTTCATTGT TAGTAATATT GGTGAATTGT	760
AATAACCTTT TAAATCTAG AGGAGAACCC AGATATAAAA	800
TGGAGGAATA TTAATGGAAA ACAATAAAA AGTATTGAAG	840
AAAATGGTAT TTTTGTTTT AGTGACATT CTTGGACTAA	880
CAATCTCGCA AGAGGTATTT GCTCAACAAG ACCCCGATCC	920
AAGCCAACCTT CACAGATCTA GTTAGTTAA AAACCTTCAA	960
AATATATATT TTCTTTATGA GGGTGACCT GTTACTCACG	1000
AGAATGTGAA ATCTGTTGAT CAACTTAGAT CTCACGATT	1040
AATATATAAT GTTTCAGGGC CAAATTATGA TAAATTAAAA	1080
ACTGAACCTTA AGAACCAAGA GATGGCAACT TTATTTAAGG	1120
ATAAAAACGT TGATATTTAT GGTGTAGAAT ATTACCATCT	1160
CTGTTATTTA TGTGAAAATG CAGAAAGGAG TGCATGTATC	1200
TACGGAGGGG TAACAAATCA TGAAAGGAAT CATTAGAAA	1240
TTCCTAAAAA GATAGTCGTT AAAGTATCAA TCGATGGTAT	1280
CCAAAGCCTA TCATTTGATA TTGAAACAAA TAAAAAAATG	1320
GTAACTGCTC AAGAATTAGA CTATAAAGTT AGAAAATATC	1360
TTACAGATAA TAAGCAACTA TATACTAATG GACCTTCTAA	1400
ATATGAAACT GGATATATAA AGTCATACC TAAGAATAAA	1440
GAAAGTTTTT GGTTTGATTT TTTCCCTGAA CCAGAATTAA	1480
CTCAATCTAA ATATCTTATG ATATATAAAG ATAATGAAAC	1520
GCTTGACTCA AACACAAGCC AAATTGAAGT CTACCTAAC	1560
ACCAAGTAAC TTTTGCTTT TGGCAACCTT ACCTACTGCT	1600
GGATTAGAA ATTTTATTGC AATTCTTTA TTAATGTAAA	1640
AACCGCTCAT TTGATGAGCG GTTTGTCTT ATCTAAAGGA	1680
GCTTTACCTC CTAATGCTGC AAAATTTAA ATGTTGGATT	1720
TTTGTATTTG TCTATTGTAT TTGATGGGTA ATCCCATT	1760
TCGACAGACA TCGTCGTGCC ACCTCTAACCA CAAAATCAT	1800

AGACAGGAGC TTGTAGCTTA GCAACTATTT TATCGTC

1837

(17) INFORMATION FOR SEQUENCE ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Glu	Asn	Asn
5	Lys	Lys	Val
		Leu	Lys

Met	Val	Phe	Phe
15	Val	Leu	Val
	Thr	Phe	Leu

Gly	Leu	Thr	Ile
25	Ser	Gln	Glu
	Val		Phe
			Ala

Gln	Gln	Asp	Pro
35	Asp	Pro	Asp
			Pro
			Ser

Arg	Ser	Ser	Leu
45	Val	Lys	Asn
		Leu	Gln
			Asn

Ile	Tyr	Phe	Leu
55	Tyr	Glu	Gly
		Asp	Pro
			Val

Thr	His	Glu	Asn
65	Val	Lys	Ser
		Val	Asp
			Gln

Leu	Arg	Ser	His
75	Asp	Leu	Ile
		Tyr	Asn
			Val

Ser	Gly	Pro	Asn
85	Tyr	Asp	Lys
			Leu
			Lys

Glu	Leu	Lys	Asn
95	Gln	Glu	Met
			Ala
			Thr

Phe	Lys	Asp	Lys
105	Asn	Val	Asp
			Ile
			Tyr

Val	Glu	Tyr	Tyr
115	Tyr	His	Leu
		Cys	Tyr
			Leu

Glu	Asn	Ala	Glu
125	Arg	Ser	Ala
			Cys
			Ile

Gly	Gly	Val	Thr
		Asn	Asn
		His	Glu
			Asn

	135	140
Leu Glu Ile Pro Lys Lys Ile Val Val Lys		
145	150	
Val Ser Ile Asp Gly Ile Gln Ser Leu Ser		
155	160	
Phe Asp Ile Glu Thr Asn Lys Lys Met Val		
165	170	
Thr Ala Gln Glu Leu Asp Tyr Lys Val Arg		
175	180	
Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr		
185	190	
Thr Asn Gly Pro Ser Lys Tyr Glu Thr Gly		
195	200	
Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu		
205	210	
Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro		
215	220	
Glu Phe Thr Gln Ser Lys Tyr Leu Met Ile		
225	230	
Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn		
235	240	
Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr		
245	250	
Lys		

(18) INFORMATION FOR SEQUENCE ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: Unknown
 - (D) TOPOLOGY: Unknown
- (ii) Molecule type: Peptide

Ser His Asp Gln Phe Leu Gln His Thr Ile		
5	10	
Leu Phe Lys Gly Phe Phe Thr Asp His Ser		
15	20	
Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp		
25	30	
Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly		
35	40	

Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala	Tyr	Tyr
				45					50
Gly	Tyr	Gln	Cys	Ala	Gly	Gly	Thr	Pro	Asn
				55					60
Lys	Thr	Ala	Cys	Met	Tyr	Gly	Gly	Val	Thr
				65					70
Leu	His	Asp	Asn	Asn	Arg	Leu	Thr	Glu	Glu
				75					80

Lys Lys

(19) INFORMATION FOR SEQUENCE ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Thr	Gly	Asp	Gln	Phe	Leu	Glu	Asn	Thr	Leu
				5					10
Leu	Tyr	Lys	Lys	Phe	Phe	Thr	Asp	Leu	Ile
				15					20
Asn	Phe	Glu	Asp	Leu	Leu	Ile	Asn	Phe	Asn
				25					30
Ser	Lys	Glu	Met	Ala	Gln	His	Phe	Lys	Ser
				35					40
Lys	Asn	Val	Asp	Val	Tyr	Pro	Ile	Arg	Tyr
				45					50
Ser	Ile	Asn	Cys	Tyr	Gly	Gly	Glu	Ile	Asp
				55					60
Arg	Thr	Ala	Cys	Thr	Tyr	Gly	Gly	Val	Thr
				65					70
Pro	His	Glu	Gly	Asn	Lys	Leu	Lys	Glu	Arg
				75					80

Lys Lys

(20) INFORMATION FOR SEQUENCE ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser	Asp	Asp	Gln	Phe	Leu	Glu	Asn	Thr	Leu
				5					10
Leu	Phe	Lys	Gly	Phe	Phe	Thr	Gly	His	Pro
				15					20
Trp	Tyr	Asn	Asp	Leu	Leu	Val	Asp	Leu	Gly
				25					30
Ser	Lys	Asp	Ala	Thr	Asn	Lys	Tyr	Lys	Gly
				35					40
Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala	Tyr	Tyr
				45					50

Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn
 55 60
 Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
 65 70
 Leu His Asp Asn Asn Arg Leu Thr Glu Glu
 75 80
 Lys Lys

(21) INFORMATION FOR SEQUENCE ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Ile Asp Gln Phe Leu Tyr Phe Asp Leu
 5 10
 Ile Tyr Ser Ile Lys Asp Thr Lys Leu Gly
 15 20
 Asn Tyr Asp Asn Val Arg Val Glu Phe Lys
 25 30
 Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp
 35 40
 Lys Tyr Val Asp Val Phe Gly Ala Asn Tyr
 45 50
 Tyr Gln Cys Tyr Phe Ser Lys Lys Thr Asn
 55 60
 Asp Ile Asn Ser His Gln Thr Asp Lys Arg
 65 70
 Lys Thr Cys Met Tyr Gly Gly Val Thr Glu
 75 80
 His Asn Gly Asn Gln Leu Asp Lys Tyr
 85

(22) INFORMATION FOR SEQUENCE ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Lys Phe Leu Ala His Asp Leu
 5 10
 Ile Tyr Asn Ile Ser Asp Lys Lys Leu Lys
 15 20
 Asn Tyr Asp Lys Val Lys Thr Glu Leu Leu
 25 30
 Asn Glu Gly Leu Ala Lys Lys Tyr Lys Asp
 35 40
 Glu Val Val Asp Val Tyr Gly Ser Asn Tyr
 45 50
 Tyr Val Asn Cys Tyr Phe Ser Ser Lys Asp

	55	60							
Asn	Val	Gly	Lys	Val	Thr	Gly	Gly	Lys	Thr
	65								70
Cys	Met	Tyr	Gly	Gly	Ile	Thr	Lys	His	Glu
	75								80
Gly	Asn	His	Phe	Asp	Asn	Gly	Asn	Leu	
	85								

(23) INFORMATION FOR SEQUENCE ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser	Val	Asp	Lys	Phe	Leu	Ala	His	Asp	Leu
				5					10
Ile	Tyr	Asn	Ile	Ser	Asp	Lys	Lys	Leu	Lys
				15					20
Asn	Tyr	Asp	Lys	Val	Lys	Thr	Glu	Leu	Leu
				25					30
Asn	Glu	Asp	Leu	Ala	Lys	Lys	Tyr	Lys	Asp
				35					40
Glu	Val	Val	Asp	Val	Tyr	Gly	Ser	Asn	Tyr
				45					50
Tyr	Val	Asn	Cys	Tyr	Phe	Ser	Ser	Lys	Asp
				55					60
Asn	Val	Gly	Lys	Val	Thr	Gly	Gly	Lys	Thr
				65					70
Cys	Met	Tyr	Gly	Gly	Ile	Thr	Lys	His	Glu
				75					80
Gly	Asn	His	Phe	Asp	Asn	Gly	Asn	Leu	
	85								

(24) INFORMATION FOR SEQUENCE ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser	Val	Asp	Lys	Phe	Leu	Ala	His	Asp	Leu
				5					10
Ile	Tyr	Asn	Ile	Ser	Asp	Lys	Lys	Leu	Lys
				15					20
Asn	Tyr	Asp	Lys	Val	Lys	Thr	Glu	Leu	Leu
				25					30
Asn	Glu	Asp	Leu	Ala	Lys	Lys	Tyr	Lys	Asp
				35					40
Glu	Val	Val	Asp	Val	Tyr	Gly	Ser	Asn	Tyr
				45					50
Tyr	Val	Asn	Cys	Tyr	Phe	Ser	Ser	Lys	Asp
				55					60

Asn	Val	Gly	Lys	Val	Thr	Gly	Gly	Lys	Thr
				65					70
Cys	Met	Tyr	Gly	Gly	Ile	Thr	Lys	His	Glu
				75					80
Gly	Asn	His	Phe	Asp	Asn	Gly	Asn	Leu	
				85					

(25) INFORMATION FOR SEQUENCE ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser	Val	Asp	Gln	Leu	Leu	Ser	His	Asp	Leu
				5					10
Ile	Tyr	Asn	Val	Ser	Gly	Pro	Asn	Tyr	Asp
				15					20
Lys	Leu	Lys	Thr	Glu	Leu	Lys	Asn	Gln	Glu
				25					30
Met	Ala	Thr	Leu	Phe	Lys	Asp	Lys	Asn	Val
				35					40
Asp	Ile	Tyr	Gly	Val	Glu	Tyr	Tyr	His	Leu
				45					50
Cys	Tyr	Leu	Cys	Glu	Asn	Ala	Glu	Arg	Ser
				55					60
Ala	Cys	Ile	Tyr	Gly	Gly	Val	Thr	Asn	His
				65					70
Glu	Gly	Asn	His	Leu	Glu	Ile	Pro	Lys	
				75					

(26) INFORMATION FOR SEQUENCE ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Val	Leu	Asp	Asn	Ser	Leu	Gly	Ser	Met	Arg
					5				10
Ile	Lys	Asn	Thr	Asp	Gly	Ser	Ile	Ser	Leu
				15					20
Ile	Ile	Phe	Pro	Ser	Pro	Tyr	Tyr	Ser	Pro
				25					30
Ala	Phe	Thr	Lys	Gly	Glu	Lys	Val	Asp	Leu
				35					40
Asn	Thr	Lys	Arg	Thr	Lys	Lys	Ser	Gln	His
				45					50
Thr	Ser	Glu	Gly	Thr	Tyr	Ile	His	Phe	Gln
				55					60
Ile	Ser	Gly	Val	Thr	Asn	Thr	Glu	Lys	Leu
				65					70
Pro	Thr	Pro							